

Abstract

A protease having two aspartate residues in a catalytically active structure, wherein a first aspartate residue resides in an X_1GX_2GD motif and a second aspartate residue resides in an $X_3X_4DX_5$ motif, wherein X_1 , X_2 , X_3 and X_5 are independently selected from Ala, Val, Leu, Met and Ile, and X_4 is an aromatic amino acid, and the motifs X_1GX_2GD and $X_3X_4DX_5$ reside in a transmembrane region.